Propositions belonging to:

Multi-omics strategies for detecting gene-environment interactions

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1. 1+1≥2; integration of multiple datasets enables analyses not possible in individual datasets. (this thesis)

2. Allelic imbalance of RNA-seq data can reveal regulatory effects of rare pathogenic variants. (this thesis)

3. Changes in DNA methylation can reveal the downstream effects of genetic risk factors. (this thesis)

4. The environmental component of complex disease development can be mediated through altered gene regulation. (this thesis)

5. Regulatory effects of disease-associated variants are not driven by random co-localization. (this thesis)

6. Large-scale population transcriptomics can be used to aid the interpretation of diagnostic genome sequencing. (this thesis)

7. In the near future, genetic profiling will be requested via a general practitioner and will become part of standard newborn screening.

8. High-density molecular profiling, such as transcriptomics, metabolomics, and microbiomics, will become standards tools of medical specialists allowing personalized medicine.

9. BBMRI-NL and Lifelines show that large-scale infrastructure projects and biobanking efforts are essential to develop the methods needed for personalized medicine.

10. For personalized medicine to be successful, we need to collaborate.

11. All countries should have their own biobanks to reflect their genetic diversity and environmental factors.

12. Nothing in biology makes sense except in the light of evolution. (Theodosius Dobzhansky)